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(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing  
the Proteins

(iii) NUMBER OF SEQUENCES: 108

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
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(C) REFERENCE/DOCKET NUMBER: FJN-060

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..14

(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..12

(D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids

- (B) ~~NAME~~ amino acid  
(C) ~~STABILITY~~:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..380  
(D) OTHER INFORMATION: /note= "(OCIF protein without signal peptide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His  
1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His  
20 25 30

Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr  
35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
65 70 75 80

Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
115 120 125

Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
130 135 140

Cys Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
145 150 155 160

Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
165 170 175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
180 185 190

Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
210 215 220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
225 230 235 240

Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
245 250 255

Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
260 265 270

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
 290 295 300  
 Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
 305 310 315 320  
 Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe  
 325 330 335  
 Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
 340 345 350  
 Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
 355 360 365  
 Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..380
  - (D) OTHER INFORMATION: /note= "(OCIF protein)"
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
  - (D) OTHER INFORMATION: /note= "(signal peptide)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp.  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Ile Ala Gly Thr Pro Glu Arg Asn Thr Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn  
300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Thr  
335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
350 355 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
365 370 375

Leu  
380

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1206

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGACACCCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "(a N-terminal amino acid sequence of the protein)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1185 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCTCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGTGC	AATCGCACCC	ACAACCGCGT	GTGCGAATGC	300
AAGGAAGGGC	GCTACCTTGA	GATAGAGTTC	TGCTTGAAAC	ATAGGAGCTG	CCCTCCTGGA	360
TTTGGAGTGG	TGCAAGCTGG	AAACCCAGAG	CGAAATACAG	TTTGCAAAAG	ATGTCCAGAT	420
GGGTTCTTCT	CAAATGAGAC	GTCATCTAAA	GCACCCCTGTA	GAAAACACAC	AAATTGCAGT	480
GTCTTGGTC	TCCTGCTAAC	TCAGAAAGGA	AATGCAACAC	ACGACAACAT	ATGTTCCGGA	540
AACAGTGAAT	CAACTCAAAA	ATGTGGAATA	GATGTTACCC	TGTGTGAGGA	GGCATTCTTC	600
AGGTTTGCTG	TTCCCTACAAA	GTTCACGCCT	AACTGGCTTA	GTGTCTTGGT	AGACAATTG	660
CCTGGCACCA	AAGTAAACGC	AGAGAGTGT	GAGAGGATAA	AACGGCAACA	CAGCTCACAA	720
GAACAGACTT	TCCAGCTGCT	GAAGTTATGG	AAACATCAA	ACAAAGACCA	AGATATAGTC	780
AAGAAGATCA	TCCAAGATAT	TGACCTCTGT	GAAAACAGCG	TGCAGCGGCA	CATTGGACAT	840
GCTAACCTCA	CCTTCGAGCA	GCTTCGTAGC	TTGATGGAAA	GCTTACCGGG	AAAGAAAGTG	900
GGAGCAGAAG	ACATTGAAAA	AACAATAAAG	GCATGCAAAC	CCAGTGACCA	GATCCTGAAG	960
CTGCTCAGTT	TGTGGCGAAT	AAAAAAATGGC	GACCAAGACA	CCTTGAAGGG	CCTAATGCAC	1020
GCACCAAAGC	ACTCAAAGAC	GTACCACTTT	CCCAAAACTG	TCACTCAGAG	TCTAAAGAAG	1080
ACCATCAGGT	TCCTTCACAG	CTTCACAATG	TACAAATTGT	ATCAGAAGTT	ATTTTTAGAA	1140
ATGATAGGTA	ACCAGGTCCA	ATCAGTAAAA	ATAAGCTGCT	TATAA		1185

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys Asn Arg Thr His Asn Arg  
60 65 70 75

Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu  
80 85 90

Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr  
95 100 105

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser  
110 115 120

Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser  
125 130 135

Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn  
140 145 150 155

Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val  
160 165 170

Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe  
175 180 185

Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys  
190 195 200

Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln  
205 210 215

Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp  
220 225 230 235

Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn  
240 245 250

Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu

Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp
270								275				280			
Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys
285								290				295			
Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys
300					305				310			315			
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys
320								325				330			
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe
335								340				345			
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn
350								355				360			
Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu						
365								370							

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1089 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: -
  - (B) LOCATION: 1..1089
  - (D) OTHER INFORMATION: /note= "(OCIF3)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAACAAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTGTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAAACACA	CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTG	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780

AACAAAGACC AA	TAC-T	CAAGAAGATC ATCCAAGATA TTGAC	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC AGTTGTGGC	GAATAAAAAA TGGCGACCAA	900
GACACCTTGA	AGGGCCTAAT	GCACGCACTA AAGCACTCAA	AGACGTACCA CTTTCCAAA	960
ACTGTCACTC	AGAGTCTAAA	GAAGACCATC AGGTTCCCTTC	ACAGCTTCAC AATGTACAAA	1020
TTGTATCAGA	AGTTATTTT	AGAAATGATA GGTAACCAGG	TCCAATCAGT AAAAATAAGC	1080
TGCTTATAA				1089

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: /note= "(OCIF3)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly	Asn	Ala	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Arg	Glu	Ser	Thr	
160														170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
175															185
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
190															200
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
205															215
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
220															235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
240															250
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
255															265
Asn	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys
270															280
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys
285															295
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe
300															315
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn
320															330
Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu						
335															340

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: /note= "(OCIF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAACAAAGT	TGCTGTGCTG	CTCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GTACGTGTCA	ATGTGCAGCA	420

AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTTAG

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: /note= "(OCIF4)"

(ix) FEATURE:
 

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ser	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
															-10
-20															
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
															10
-5						1				5					
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
															25
15										20					
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
															40
30						35									
Cys	Pro	Asp	His	Tyr	Tyr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
45						50									
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
															75
60						65				70					
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
															90
80										85					
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
															105
95										100					
Gly	Val	Val	Gln	Ala	Gly	Thr	Cys	Gln	Cys	Ala	Ala	Lys	Leu	Ile	Arg
															120
110										115					
Ile	Met	Gln	Ser	Gln	Ile	Val	Val	Thr	Val						
125															

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 438 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..438  
(D) OTHER INFORMATION: /note= "(OCIF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAACAAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAAACACT GTACAGCAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GATGCAGGAG AAGACCCAAG	420
CCACAGATAT GTATCTGA	438

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: /note= "(OCIF5)"

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile			
-20	-15	-10	
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp			
-5	1	5	10
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr			
15	20	25	
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro			
30	35	40	
Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys			
45	50	55	
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu			
60	65	70	75
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr			
80	85	90	
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe			

Gly Val Val Gln Ala Gly Cys Arg Arg Arg Pro Lys Pro Gln Ile Cys  
 110 115 120

Ile

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCTT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCAC TATA GG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGTCCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTATTCGCCA CAAACTGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATGAACAAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

(xi) SEQUE~~RE~~ DESCRIPTION: SEQ ID NO:25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTAGGTAC CAGGAGGACA

20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCTGCCCT CCTGGATTG

20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAACGTAT TTTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..20  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer C19SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer C19SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTAACATCTA TTCCACTTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C20SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGATGTTA CCCTGAGTGA GGAGGCATTC

30

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C20SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATGCCTCC TCACTCAGGG TAACATCTAT

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C21SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGATATTG ACCTCAGTGA AAACAGCGTG C

31

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -

(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C21SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCACGCTGTT TTCACTGAGG GCAATATCTT G

31

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C22SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAACAATAA AGGCAAGCAA ACCCAGTGAC C

31

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C22SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTCACTGGG TTTGCTTGCC TTTATTGTTT T

31

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer  
C23SF)"

(xi) SEQUENCER DESCRIPTION: SEQ ID NO:38:

TCAGTAAAAA TAAGCAGCTT ATAACGGCC A

31

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..31  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer C23SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCAGTTA TAAGCTGCTT ATTTTTACTG A

31

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF14)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGGGGTTTA TTGGAGGAGA TG

22

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCAGGGCAA GGTTCCCTGGG TGGTCCACTT AATGGA

36

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGTGTGCG CGGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTCCTTGCAT TCGGCGCACCA CGGTCTTCCA CTTTGC

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR3F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACCGCGTGT GCAGATGTCC AGATGGGTTTC TTCTCA

36

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR3R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTGGACAT CTGCACACGC GGTTGTGGGT GCGATT

36

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAGTTGCA AATCCGGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTGTTCCG GATTTGCAAA CTGTATTCG CTCTGG

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGAGGTCAAT ATCTATTCCA CATTGGAG TTGATT

36

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCTTTAGTGC GTCTTGGATG ATCTTCTTGA CTATAT

36

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoI F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF16)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTGAGTGCT TTAGTGCCTG

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CL F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCAGTAAAAAA TAAGCTAACT GGAAATGGCC

30

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CL R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCCATTTCG AGTTAGCTTA TTTTTACTGA

30

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CC R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGATCCTC AGTGCTTAG TGCGTGCAT

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCGGATCCTC ATATTCCACA TTTTGAGT

29

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGGATCCTC ATTTGCAAAC TGTATTCG

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..29  
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR3  
R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCGGATCCTC ATTGCACAC GCGGTTGTG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 401 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..380  
(D) OTHER INFORMATION: /note= "OCIF-C19S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr

160  
 Gln Lys Ser Gly Ile Asp Val Thr Leu Cys Glu Ala Phe Phe Arg  
 175 180 185  
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 365 370 375

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 401 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: -21..0
  - (ix) FEATURE:
    - (A) NAME/KEY: Protein
    - (B) LOCATION: 1..380
    - (D) OTHER INFORMATION: /note= "OCIF-C20S"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Ser Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345

Ile Arg Phe His Ser Phe Thr Met Tyr Lys Leu Gln Lys Leu  
350 355

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
365 370 375

Leu  
380

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C21S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160 165 170

Gln Lys Cys [REDACTED] Ile Asp Val Thr Leu Cys Glu Glu [REDACTED] Phe Phe Arg  
180 [REDACTED] 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
240 245 250

Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
350 355 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
365 370 375

Leu  
380

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C22S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Th Gln Glu Thr Phe Pro Pro Lys Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Lys  
 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360

Phe Leu Gln Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
365 370 375

Leu  
380

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 401 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..380  
(D) OTHER INFORMATION: /note= "OCIF-C23S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200  
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215  
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235  
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Ser  
 365 370 375  
 Leu  
 380

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 360 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..339
  - (D) OTHER INFORMATION: /note= "OCIF-DCR1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10  
 Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser  
 -5 1 5 10

Trp His ~~T~~ Ser Asp Glu Cys Leu Tyr Cys Ser ~~H~~ Val Cys Lys Glu  
 15 20 25

Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys  
 30 35 40

Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His  
 45 50 55

Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu  
 60 65 70 75

Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu  
 80 85 90

Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe  
 95 100 105

Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys  
 110 115 120

Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu  
 125 130 135

Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro  
 140 145 150 155

Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn  
 160 165 170

Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln  
 175 180 185

Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp  
 190 195 200

Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val  
 205 210 215

Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser  
 220 225 230 235

Leu Met Glu Ser Leu Pro Gly Lys Val Gly Ala Glu Asp Ile Glu  
 240 245 250

Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu  
 255 260 265

Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu  
 270 275 280

Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val  
 285 290 295

Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met  
 300 305 310 315

Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val  
 320 325 330

Gln Ser Val Lys Ile Ser Cys Leu  
 335

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 amino acids

- (B) The ~~amino~~ amino acid  
(C) STRAIGHTNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..338  
(D) OTHER INFORMATION: /note= "OCIF-DCR2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Glu  
30 35 40

Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg  
45 50 55

Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg  
60 65 70 75

Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr  
80 85 90

Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly  
95 100 105

Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser  
110 115 120

Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
125 130 135

Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
140 145 150 155

Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
160 165 170

Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr  
175 180 185

Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile  
190 195 200

Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln  
205 210 215

Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu  
220 225 230 235

Met Glu Ser Leu Pro Gly Lys Val Gly Ala Glu Asp Ile Glu Lys

Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser  
 255 260 265  
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met  
 270 275 280  
 His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
 285 290 295  
 Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
 300 305 310 315  
 Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
 320 325 330  
 Ser Val Lys Ile Ser Cys Leu  
 335

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 363 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:
 

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: /note= "OCIF-DCR3"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Arg Cys Pro Asp Gly Phe Phe  
 80 85 90

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys  
 95 100 105

Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp

Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp  
 125 130 135

Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys  
 140 145 150 155

Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr  
 160 165 170

Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser  
 175 180 185

Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys  
 190 195 200

Asp Gln Asp Ile Val Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu  
 205 210 215

Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln  
 220 225 230 235

Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu  
 240 245 250

Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu  
 255 260 265

Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu  
 270 275 280

Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro  
 285 290 295

Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser  
 300 305 310 315

Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly  
 320 325 330

Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
 335 340

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 359 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..338
  - (D) OTHER INFORMATION: /note= "OCIF-DCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

-20

-15

-10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Ser  
110 115 120

Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys  
125 130 135

Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn  
140 145 150 155

Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala  
160 165 170

Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr  
175 180 185

Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile  
190 195 200

Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln  
205 210 215

Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu  
220 225 230 235

Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys  
240 245 250

Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser  
255 260 265

Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met  
270 275 280

His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
285 290 295

Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
300 305 310 315

Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
320 325 330

Ser Val Lys Ile Ser Cys Leu  
335

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..305  
(D) OTHER INFORMATION: /note= "OCIF-DDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160 165 170

Gln Lys Cys Gly Ile Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg  
175 180 185

His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met  
190 195 200

Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr  
205 210 215

Ile Lys Ala **Asn** Lys Pro Ser Asp Gln Ile Leu Ly **u** Leu Ser Leu  
 220 225 230 235

Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His  
 240 245 250

Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln  
 255 260 265

Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys  
 270 275 280

Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser  
 285 290 295

Val Lys Ile Ser Cys Leu  
 300 305

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..306
- (D) OTHER INFORMATION: /note= "OCIF-DDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Phe Phe Ser Asn Glu Thr Ser Ser Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

Asp Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
 255 260 265

Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
 270 275 280

Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
 285 290 295

Ser Val Lys Ile Ser Cys Leu  
 300 305

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: /note= "OCIF-CL"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys His Cys Thr Ala Lys Trp Lys Thr Cys Ala Pro  
 30 35

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser  
 365 370 375

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: -21..0

(ix) FEATURE:  
(A) NAME/KEY: Protein  
(B) LOCATION: 1..330  
(D) OTHER INFORMATION: /note= "OCIF-CC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
-20   -15   -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
-5   1   5   10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
15   20   25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
30   35   40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
45   50   55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
60   65   70   75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
80   85   90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
95   100   105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
110   115   120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
125   130   135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
140   145   150   155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
160   165   170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
175   180   185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
190   195   200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
205   210   215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
220   225   230   235

Trp Lys His Asn Asn Lys Asp Gln Asp Ile Val Leu Lys Ile Ile Gln  
 240 245 250  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His  
 320 325 330

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..251  
 (D) OTHER INFORMATION: /note= "OCIF-CDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Ile Phe Phe Ser Asn Glu Thr Ser Ser Asn Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 197 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: -21..0
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 1..176
  - (D) OTHER INFORMATION: /note= "OCIF-CDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr

Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
95								100							105
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
	110							115							120
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125							130							135
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
	140							145				150			155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
							160				165			170	
Gln	Lys	Cys	Gly	Ile											
				175											

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: /note= "OCIF-CCR4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20									-15					-10	

Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1					5				10		

Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
15								20						25	

Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
30								35						40	

Cys	Pro	Asp	His	Tyr	Tyr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45						50						55		

Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60						65				70			75		

Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
80								85					90		

Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
95								100						105	

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: /note= "OCIF-CCR3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20															

Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5															

Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
15															

Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
30															

Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45															

Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60															

Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu						
80															

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: /note= "OCIF-CBst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Asn Asp Leu Leu Cys Cys Ala Leu Val Phe Lys Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 350 355 360

Phe Leu Glu Met Ile Gly Asn Leu Val  
 365 370

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: -21..0

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..300  
 (D) OTHER INFORMATION: /note= "OCIF-CSph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg

Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
190						195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
205						210					215				
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
220					225					230					235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
					240					245					250
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
					255					260					265
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly
						270				275					280
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Ser	Leu
						285				290					295

Asp  
300

(2) INFORMATION FOR SEQ ID NO:81:

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 84 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: -21..0
  - (ix) FEATURE:
    - (A) NAME/KEY: Protein
    - (B) LOCATION: 1..63
    - (D) OTHER INFORMATION: /note= "OCIF-CPst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 -20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 -5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 30 35 40

Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys  
 45 50 55

Leu Tyr Leu Val  
 60

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C19S)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCCCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAAACCTAAA	AAAGTGGAAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	AAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCAACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAACT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	ATAAGCTGC	1200
TTATAAA						1206

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAA	AATGTGGAAT	AGATGTTACC	600
CTGAGTGAGG	AGGCATTCTT	CAGGTTGCT	GTTCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAA	AAACAATAAA	GGCATGCAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
TTATAAA						1206

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C21S)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180

GTGTGCGCCC CTTG	TGA CCACTACTAC ACAGACAGCT GGCACAC	TGACGAGTGT	240
CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCCGACC			300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA			360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA			420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT			480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA			540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC			600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTACAA AGTTTACGCC TAACTGGCTT			660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA			720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA			780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCAG TGAAAACAGC			840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA			900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAAA			960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC			1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAACTT TCCCCAAACT			1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTTCACA GCTTCACAAAT GTACAAATTG			1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCTGC			1200
TTATAA			1206

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1206
  - (D) OTHER INFORMATION: /note= "(OCIF-C22S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCCTCCAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCCGACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360

CATAGGAGCT GCGCTTCG-G	ATTGGAGTG GTGCAAGCTG	GAACCC	GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG	AAACAGTGAA	TCAACTCAA	AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT	CAGGTTGCT	GTTCTACAA	AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAAGT	GGGAGCAGAA	GACATTGAA	AAACAATAAA GGCAAGCAAA	960
CCCAGTGACC AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA	CGCACTAAAG	CACTCAAAGA CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA AATAAGCTGC	1200
TTATAAA				1206

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C23S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGAACAACT TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG	ATTGGAGTG	GTGCAAGCTG	GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA CGTCATCTAA	AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG	AAACAGTGAA	TCAACTCAA	AATGTGGAAT AGATGTTACC	600

CTGTGTGAGG AGGCA	TTT CAGGTTGCT GTTCCTACAA AGTTTAC	TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA			720
AAACGGCAAC ACAGCTCAC A AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA			780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC			840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA			900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAAA			960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAAATGG CGACCAAGAC			1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAACTT TCCCCAAACT			1080
GTCACACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG			1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA AATAAGCAGC			1200
TTATAA			1206

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1083
- (D) OTHER INFORMATION: /note= "(OCIF-DCR1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAACCTT GCCCTGACCA CTACTACACA GACAGCTGGC ACACCAGTGA CGAGTGTCTA	120
TACTGCAGCC CCGTGTGCAA GGAGCTGCAG TACGTCAAGC AGGAGTGCAG TCGCACCCAC	180
AACCGCGTGT GCGAATGCAA GGAAGGGCGC TACCTTGAGA TAGAGTTCTG CTTGAAACAT	240
AGGAGCTGCC CTCCTGGATT TGGAGTGGTG CAAGCTGGAA CCCCAGAGCG AAATACAGTT	300
TGCAAAAGAT GTCCAGATGG GTTCTTCTCA AATGAGACGT CATCTAAAGC ACCCTGTAGA	360
AAACACACAA ATTGCAGTGT CTTTGGTCTC CTGCTAACTC AGAAAGGAAA TGCAACACAC	420
GACAACATAT GTTCCGGAAA CAGTGAATCA ACTCAAAAT GTGGAATAGA TGTTACCTG	480
TGTGAGGAGG CATTCTTCAG GTTGCTGTT CCTACAAAGT TTACGCCTAA CTGGCTTAGT	540
GTCTTGGTAG ACAATTGCC TGGCACCAAA GTAAACGCAG AGAGTGTAGA GAGGATAAAA	600
CGGCAACACA GCTCACAAGA ACAGACTTTC CAGCTGCTGA AGTTATGGAA ACATCAAAAC	660
AAAGACCAAG ATATAGTCAA GAAGATCATC CAAGATATTG ACCTCTGTGA AAACAGCGTG	720
CAGCGCACA TTGGACATGC TAACCTCACC TTGAGCAGC TTGAGCTT GATGGAAAGC	780

TTACCGGGAA AGA[REDACTED]GCC	AGCAGAACAC ATTGAAAAAA CAATAA[REDACTED]	ATGCAAACCC	840
AGTGACCAGA TCCTGAAGCT GCTCAGTTG TGGCGAATAA AAAATGGCGA	CCAAGACACC		900
TTGAAGGGCC TAATGCACGC ACTAAAGCAC TCAAAGACGT ACCACTTCC	CAAAACTGTC		960
ACTCAGAGTC TAAAGAAGAC CATCAGGTT CTTCACAGCT TCACAATGTA	CAAATTGTAT		1020
CAGAAGTTAT TTTAGAAAT GATAGGTAAC CAGGTCCAAT CAGTAAAAT AAGCTGCTTA			1080
TAA			1083

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1080
- (D) OTHER INFORMATION: /note= "(OCIF-DCR2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCG AATGCAAGGA AGGGCGCTAC CTTGAGATAG AGTTCTGCTT GAAACATAGG	240
AGCTGCCCTC CTGGATTGAG AGTGGTGCAA GCTGGAACCC CAGAGCGAAA TACAGTTGC	300
AAAAGATGTC CAGATGGGTT CTTCTCAAAT GAGACGTCACT CTAAAGCACC CTGTAGAAAA	360
CACACAAATT GCAGTGTCTT TGGTCTCCTG CTAACTCAGA AAGGAAATGC AACACACGAC	420
AACATATGTT CCGGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCTGTGT	480
GAGGAGGCAT TCTTCAGGTT TGCTGTTCT ACAAAAGTTA CGCCTAACTG GCTTAGTGTC	540
TTGGTAGACA ATTTGCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAAACGG	600
CAACACAGCT CACAAGAACCA GACTTTCCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA	660
GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTGAAAA CAGCGTGCAG	720
CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA	780
CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAAACAA TAAAGGCATG CAAACCCAGT	840
GACCAGATCC TGAAGCTGCT CAGTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG	900
AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT	960
CAGAGTCTAA AGAAGACCAT CAGGTTCCCTT CACAGCTTCA CAATGTACAA ATTGTATCAG	1020
AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA	1080

## (2) INFORMATION SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1092 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: /note= "(OCIF-DCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCTCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCAGATG	TCCAGATGGG	TTCTTCTCAA	ATGAGACGTC	ATCTAAAGCA	360
CCCTGTAGAA	AACACACAAA	TTGCAGTGTG	TTTGGTCTCC	TGCTAACTCA	GAAAGGAAAT	420
GCAACACACG	ACAACATATG	TTCCGGAAAC	AGTGAATCAA	CTCAAAAATG	TGGAATAGAT	480
GTTACCTGT	GTGAGGAGGC	ATTCTTCAGG	TTTGCTGTT	CTACAAAGTT	TACGCCAAC	540
TGGCTTAGTG	TCTTGGTAGA	CAATTTGCCT	GGCACCAAAG	TAAACGCAGA	GAGTGTAGAG	600
AGGATAAAAC	GGCAACACAG	CTCACAAGAA	CAGACTTCC	AGCTGCTGAA	GTTATGGAAA	660
CATCAAAACA	AAGACCAAGA	TATAGTCAG	AAGATCATCC	AAGATATTGA	CCTCTGTGAA	720
AACAGCGTGC	AGCGGCACAT	TGGACATGCT	AACCTCACCT	TCGAGCAGCT	TCGTAGCTTG	780
ATGGAAAGCT	TACCGGGAAA	GAAAGTGGGA	GCAGAAGACA	TTGAAAAAAC	AATAAAGGCA	840
TGCAAAACCA	GTGACCAGAT	CCTGAAGCTG	CTCAGTTGT	GGCGAATAAA	AAATGGCGAC	900
CAAGACACCT	TGAAGGGCCT	AATGCACGCA	CTAAAGCACT	CAAAGACGTA	CCACTTTCCC	960
AAAAGTGTCA	CTCAGAGTCT	AAAGAAGACC	ATCAGGTTCC	TTCACAGCTT	CACAATGTAC	1020
AAATTGTATC	AGAAGTTATT	TTTAGAAATG	ATAGGTAACC	AGGTCCAATC	AGTAAAATA	1080
AGCTGCTTAT	AA					1092

## (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1080 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..1080  
 (D) OTHER INFORMATION: /note= "(OCIF-DCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCTGTA	CCACTACTAC	ACAGACAGCT	GGCACACCA	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAT	CCGGAAACAG	TGAATCAACT	AAAAAATGTG	GAATAGATGT	TACCTGTGT	480
GAGGAGGCAT	TCTTCAGGTT	TGCTGTTCC	ACAAAGTTA	CGCCTAACTG	GCTTAGTGT	540
TTGGTAGACA	ATTTGCCTGG	CACCAAAGTA	AACGCAGAGA	GTGTAGAGAG	GATAAACCGG	600
CAACACAGCT	CACAAGAAC	GACTTCCAG	CTGCTGAAGT	TATGGAAACA	TCAAAACAAA	660
GACCAAGATA	TAGTCAAGAA	GATCATCCAA	GATATTGACC	TCTGTGAAA	CAGCGTGCAG	720
CGGCACATTG	GACATGCTAA	CCTCACCTTC	GAGCAGCTTC	GTAGCTTGAT	GGAAAGCTTA	780
CCGGGAAAGA	AAAGTGGGAGC	AGAAGACATT	AAAAAAACAA	TAAAGGCATG	CAAACCCAGT	840
GACCAGATCC	TGAAGCTGCT	CAGTTGTGG	CGAATAAAA	ATGGCGACCA	AGACACCTTG	900
AAGGGCCTAA	TGCACGCACT	AAAGCACTCA	AAGACGTACC	ACTTTCCAA	AACTGTCACT	960
CAGAGTCTAA	AGAAGACCAT	CAGGTTCC	CACAGCTTCA	CAATGTACAA	ATTGTATCAG	1020
AAGTTATTTT	TAGAAATGAT	AGGTAACCA	GTCCAATCAG	TAAAAATAAG	CTGCTTATAAA	1080

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
 (B) LOCATION: 1..981  
 (D) OTHER INFORMATION: /note= "(OCIF-DDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120

TGTGACAAAT GTC	TGG	TACCTACCTA AAACAACACT GTACAG	GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT				240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC				300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA				360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCCAGA GCGAAATACA				420
GTGGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT				480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA				540
CACGACAACA TATGTTCCGG AACAGTGAA TCAACTCAAA AATGTGGAAT AGATATTGAC				600
CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT				660
CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGAG CAGAAGACAT TGAAAAAACAA				720
ATAAAGGCAT GCAAACCCAG TGACCAAGATC CTGAAGCTGC TCAGTTGTG GCGAATAAAA				780
AATGGCGACC AAGACACCTT GAAGGGCCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC				840
CACTTTCCA AAACTGTCAC TCAGAGTCTA AAGAAGACCA TCAGGTTCCCT TCACAGCTTC				900
ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA				960
GTAAAAATAA GCTGCTTATA A				981

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 984 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: -  
 (B) LOCATION: 1..984  
 (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAACACT GTACAGAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCCAGA GCGAAATACA	420
GTGGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600

CTGTGTGAGG AGGCAATT CAGGTTGCT GTTCCTACAA AGTTTAC	TAACTGGCTT	660
AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA		720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA		780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG		840
TACCACTTTC CCAAAACTGT CACTCAGAGT CTAAAGAAGA CCATCAGGTT CCTTCACAGC		900
TTCACAATGT ACAAAATTGTA TCAGAAGTTA TTTTAGAAA TGATAGGTAA CCAGGTCCAA		960
TCAGTAAAAA TAAGCTGCTT ATAA		984

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "(OCIF-CL)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCTGG TACCTACCTA AAACAAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020

ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAC	TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACA	GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAAGGTCC AATCAGTAAA	AATAAGCTAA	1200

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1056 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1056
- (D) OTHER INFORMATION: /note= "(OCIF-CC)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCCTCCTGG TACCTACCTA AAACAAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTGGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTGTT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTGA	1056

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 819 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCGT	480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTGCT GTTCCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAATGA	819

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..594
- (D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240

CTATACTGCA GCC	Gt6	CAAGGAGCTG CAGTACGTCA AGCAGGA	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG CGCTACCTTG AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA		420
GTTCGAAAA	GATGTCCAGA	TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT		480
AGAAAACACA	CAAATTGCAG	TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA		540
CACGACAACA	TATGTTCCGG	AAACAGTGAA TCAACTAAA AATGTGGAAT ATGA		594

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 432 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..432
  - (D) OTHER INFORMATION: /note= "(OCIF-CCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCTCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCA	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTCGAAAA	GA					432

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..321
  - (D) OTHER INFORMATION: /note= "(OCIF-CCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
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CAGGAAACGT TTCC	GTACCTTCAT TATGACGAAG AAACCTC	TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAA	GTTGGAAAGACC	180	
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240		
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300		
CACAACCGCG TGTGCGAATG A	321		

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1182
  - (D) OTHER INFORMATION: /note= "(OCIF-CBst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAA GTGGAAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCCTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAA	960
CCCAGTGACC AGATCTGAA GCTGCTCAGT TTGTGGCAGA TAAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCAACTT TCCCCAAACT	1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAAGT TATTTTTAGA AATGATAGGT AACCTAGTCT AG	1182

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 966 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..966  
(D) OTHER INFORMATION: /note= "(OCIF-CSph)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCTGTA	CCACTACTAC	ACAGACAGCT	GGCACACCA	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAAACACA	CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTGCT	GTT CCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCTAGTCTA	960
GA	CTAG					966

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 564 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..564

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGAAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTGGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCCTGT	480
AGAAAAACACA	CAAATTGCAG	TGTCTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	CTAG				564

## (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /note= "(OCIF-Pst)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGAAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAAG	TGACGAGTGT	240
CTATACTTAG	TCTAG					255

## (2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1317

(D) OTHER INFORMATION: /note= "human OCLN genomic DNA-1"

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1173..1202
- (D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAGACAT ATAACATTGAA CACTTGGCCC TGATGGGAA GCAGCTCTGC AGGGACTTTT	60
TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA	120
CACTTTACAA GTCATCAAGT CTAACCTCTA GACCAGGGAA TTAATGGGG AGACAGCGAA	180
CCCTAGAGCA AAGTGCCAAA CTTCTGTCGA TAGCTTGAGG CTAGTGAAA GACCTCGAGG	240
AGGCTACTCC AGAAGTTCAAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG	300
TGGGGTGGT GAAGGAAACA GTGCTCCGCA AGGTATCCC TGCCCCAGGC AGTCCAATTT	360
TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT	420
AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG	480
TAAACTTGAA GATGAATGAT TGCGAACTCC CCGAAAAGGG CTCAGACAAT GCCATGCATA	540
AAGAGGGGCC CTGTAATTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGT	600
ACGGCGGAAA CTCACAGCTT TCGCCCAGCG AGAGGACAAA GGTCTGGAC ACACCTCAAC	660
TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT	720
GCCCAGCGTG TGCCCAAGCCC TCCCACCGCT GGTCCCGGCT GCCAGGAGGC TGGCCGCTGG	780
CGGGAAAGGGG CCGGGAAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCCTCAGC	840
CCGGTGGCTT TTTTTTCCCC TGCTCTCCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC	900
GCCCCACCTC CCTGGGGGAT CCTTCCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT	960
TCTGCACACC CCCCAGCCGC TCCCGCCCAA GCTTCCTAAA AAAGAAAGGT GCIAAGTTG	1020
GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCAGATA TTCCTGTTGC CGGGACGCTA	1080
TATATAACGT GATGAGCGCA CGGGCTGCCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG	1140
CCTCCAAGCC CCTGAGGTTT CGGGGGACCA CAATGAACAA GTTGCTGTGC TGCGCGCTCG	1200
TGGTAAGTCC CTGGGCCAGC CGACGGGTGC CCGGCGCCTG GGGAGGCTGC TGCCACCTGG	1260
TCTCCCAACC TCCCAGCGGA CGGGCGGGGA AAAAGGCTCC ACTCGCTCCC TCCCAAG	1317

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 130..162

(D) **FEATURE INFORMATION:** /note= "amino acid residues -11 to -1"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(130..162, 163..498, 4503..4694, 6715..6939, 8960..9346)

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: join(163..498, 4503..4694, 6715..6939, 8960..9346)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT	60
ACTGTTGCAC ATAAGAACAA ACCTATTTTC ATGCTAAGAT GATGCCACTG TGTTCCCTTC	120
TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr -11 -10 -5 1	168
TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu 5 10 15	216
TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr 20 25 30	264
GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr 35 40 45 50	312
GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys 55 60 65	360
AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg 70 75 80	408
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu 85 90 95	456
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala 100 105 110	498
GGTACGTGTC AATGTGCAGC AAAATTAATT AGGATCATGC AAAGTCAGAT AGTTGTGACA	558
GTTTAGGAGA ACACCTTTGT TCTGATGACA TTATAGGATA GCCTTGCA AAGGTAATGA	618
AACCTGCCAG GTAGGTACTA TGTGTCTGGA GTGCTTCAA AGGACCATTG CTCAGAGGAA	678
TACTTGCCTA CTACAGGGCA ATTTAATGAC AAATCTCAA TGCAGCAAAT TATTCTCTCA	738
TGAGATGCAT GATGGTTTTT TTTTTTTTT TTAAAGAAC AAACCTCAAGT TGCACATTG	798
ATAGTTGATC TATACCTCTA TATTCACCT CAGCATGGAC ACCTTCAAAC TGCAGCACCT	858
TTTGACAAAC ATCAGAAATG TTAATTATA CCAAGAGAGT AATTATGCTC ATATTAATGA	918
GACTCTGGAG TGCTAACAAAT AAGCAGTTAT ATTAATTAT GTAAAAAATG AGAATGGTGA	978
GGGAAATTGC ATTTCATTAT TAAAAACAAG GCTAGTTCTT CCTTTAGCAT GGGAGCTGAG	1038

TGTTTGGGAG GGTACACT	ATAGCAGAAT CTCTTCATG AGCTTAT	TTATCTTAGA	1098
CAAAACAGAT TGTCTGCCA	AGAGCAAGCA CTTGCCTATA AACCAAG	TTTCTTTTT	1158
GCATTTGAA CAGCATTGGT	CAGGGCTCAT GTGTATTGAA TCTTTAAAC CAGTAACCCA		1218
CGTTTTTTT CTGCCACATT	TGCGAAGCTT CAGTCAGCC TATAACTTT CATAGCTTGA		1278
GAAAATTAAG AGTATCCACT	TACTTAGATG GAAGAAGTAA TCAGTATAGA TTCTGATGAC		1338
TCAGTTGAA GCAGTGTTTC	TCAACTGAAG CCCTGCTGAT ATTTAAGAA ATATCTGGAT		1398
TCCTAGGCTG GACTCCTTT	TGTGGCAGC TGTCTGCGC ATTGTAGAAT TTTGGCAGCA		1458
CCCCCTGGACT CTAGCCACTA	GATACCAATA GCAGTCCTTC CCCCATGTGA CAGCCAAAAA		1518
TGTCTTCAGA CACTGTCAA	TGTCGCCAGG TGGCAAAATC ACTCCTGGTT GAGAACAGGG		1578
TCATCAATGC TAAGTATCTG	TAACTATTTT AACTCTAAA ACTTGTGATA TACAAAGTCT		1638
AAATTATTAG ACACCAATA	CTTTAGGTTT AAAGGCATAC AAATGAAACA TTCAAAAATC		1698
AAAATCTATT CTGTTCTCA	AATAGTGAAT CTTATAAAAT TAATCACAGA AGATGCAAAT		1758
TGCATCAGAG TCCCTTAAAAA	TTCCCTTTCG TATGAGTATT TGAGGGAGGA ATTGGTGATA		1818
GTTCCTACTT TCTATTGGAT	GGTACTTTGA GACTCAAAAG CTAAGCTAAG TTGTGTGTGT		1878
GTCAGGGTGC GGGGTGTGGA	ATCCCATCAG ATAAAAGCAA ATCCATGTAA TTCATTCACT		1938
AAGTTGTATA TGTAGAAAAA	TGAAAAGTGG GCTATGCAGC TTGGAAACTA GAGAATTTC		1998
AAAAATAATG GAAATCACAA	GGATCTTCT TAAATAAGTA AGAAAATCTG TTTGTAGAAT		2058
GAAGCAAGCA GGCAGCCAGA	AGACTCAGAA CAAAAGTACA CATTTCACACT TGTGTACACT		2118
GGCAGCACAG TGGGATTTAT	TTACCTCTCC CTCCCTAAAA ACCCACACAG CGGTTCCCTCT		2178
TGGGAAATAA GAGGTTTCCA	GCCCCAAAGAG AAGGAAAGAC TATGTGGTGT TACTCTAAAA		2238
AGTATTAAAT AACCGTTTG TTGTTGCTGT	TGCTGTTTG AAATCAGATT GTCTCCTCTC		2298
CATATTTTAT TTACTTCATT	CTGTTAACCC CTGTGGAATT ACTTAGAGCA AGCATGGTGA		2358
ATTCTCAACT GTAAAGCCAA	ATTCTCCAT CATTATAATT TCACATTTG CCTGGCAGGT		2418
TATAATTTCAT ATATTTCCAC	TGATAGTAAT AAGGTAAAAT CATTACTTAG ATGGATAGAT		2478
CTTTTCATA AAAAGTACCA	TCAGTTATAG AGGGAAAGTCA TGTTCATGTT CAGGAAGGTC		2538
ATTAGATAAA GCTTCTGAAT	ATATTATGAA ACATTAGTTC TGTCATTCTT AGATTCTTTT		2598
TGTTAAATAA CTTAAAAGC	TAACCTACCT AAAAGAAATA TCTGACACAT ATGAACCTCT		2658
CATTAGGATG CAGGAGAAGA	CCCAAGCCAC AGATATGTAT CTGAAGAATG AACAAAGATT		2718
TTAGGCCCGG CACGGTGGCT	CACATCTGTA ATCTCAAGAG TTTGAGAGGT CAAGGCCGG		2778
AGATCACCTG AGGTCAAGGAG	TTCAAGACCA GCCTGGCCAA CATGATGAAA CCCTGCCTCT		2838
ACTAAAAATA CAAAAATTAG	CAGGGCATGG TGGTGCATGC CTGCAACCCT AGCTACTCAG		2898
GAGGCTGAGA CAGGAGAATC	TCTTGAAACCC TCGAGGCGGA GGTTGTGGTG AGCTGAGATC		2958
CCTCTACTGC ACTCCAGCCT	GGGTGACAGA GATGAGACTC CGTCCCTGCC GCCGCCCG		3018
CCTCCCCCCC CAAAAAGATT	CTTCTTCATG CAGAACATAC GGCAGTCAAC AAAGGGAGAC		3078

CTGGGTCCAG GTG	AATGCCATGG	3138
AATCCCTGCC CAAATACCTC TGCTTATGAT ATTGTAGAAT TTGATATAGA GTTGATATCCC		3198
ATTTAAGGAG TAGGATGTAG TAGGAAAGTA CTAAAAACAA ACACACAAAC AGAAAACCC		3258
CTTTCCTTGC TAAGGTGGTT CCTAAGATAA TGTCAGTGCA ATGCTGGAAA TAATATTTAA		3318
TATGTGAAGG TTTTAGGCTG TGTTTCCCC TCCTGTTCTT TTTTCTGCC AGCCCTTGT		3378
CATTTTGCA GGTCAATGAA TCATGTAGAA AGAGACAGGA GATGAAACTA GAACCAGTCC		3438
ATTTTGCCTTCTTATT TTCTGGTTTT GGAAAAGAT ACAATGAGGT AGGAGGTTGA		3498
GATTTATAAA TGAAGTTAA TAAGTTCTG TAGCTTGAT TTTCTCTT CATATTTGTT		3558
ATCTTGCATA AGCCAGAATT GGCCTGTAAA ATCTACATAT GGATATTGAA GTCTAAATCT		3618
GTTCAACTAG CTTACACTAG ATGGAGATAT TTTCATATTC AGATACACTG GAATGTATGA		3678
TCTAGCCATG CGTAATATAG TCAAGTGTGTT GAAGGTATT ATTGTTAATA GCGTCTTGT		3738
TTGTGGACTG GTTCAAGTTT TTCTGCCAAT GATTCTTCA AATTTATCAA ATATTTTCC		3798
ATCATGAAGT AAAATGCCCT TGCAGTCACC CTTCCGTGAAG TTTGAACGAC TCTGCTGTT		3858
TAAACAGTTT AAGCAAATGG TATATCATCT TCCGTTACT ATGTAGCTTA ACTGCAGGCT		3918
TACGCTTTG AGTCAGCGGC CAACTTATT GCCACCTTCA AAAGTTTATT ATAATGTTGT		3978
AAATTTTAC TTCTCAAGGT TAGCATACTT AGGAGTTGCT TCACAATTAG GATTCAAGGAA		4038
AGAAAGAACT TCAGTAGGAA CTGATTGGAA TTTAATGATG CAGCATTCAA TGGGTACTAA		4098
TTTCAAAGAA TGATATTACA GCAGACACAC AGCAGTTATC TTGATTTCT AGGAATAATT		4158
GTATGAAGAA TATGGCTGAC AACACGGCCT TACTGCCACT CAGCGGAGGC TGGACTAATG		4218
AACACCCCTAC CCTTCTTCC TTTCCCTCTCA CATTTCATGA GCGTTTTGTA GGTAACGAGA		4278
AAATTGACTT GCATTTGCAT TACAAGGAGG AGAAACTGGC AAAGGGGATG ATGGTGGAAAG		4338
TTTTGTTCTG TCTAATGAAG TGAAAATGA AAATGCTAGA GTTTTGTCACATAATAGT		4398
AGCAGTAAAA ACCAAGTGAA AAGTCTTCC AAAACTGTGT TAAGAGGGCA TCTGCTGGGA		4458
AACGATTGAA GGAGAAGGTA CTAAATTGCT TGGTATTTTC CGTA GGA ACC CCA GAG		4514
Gly Thr Pro Glu		
115		
CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG		4562
Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu		
120 125 130		
ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT		4610
Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe		
135 140 145		
GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT		4658
Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys		
150 155 160		
TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT GGA ATA GGTAATTACA		4704
Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile		
165 170 175		
TTCCAAAATA CGTCTTGTGTA CGATTTGTGTA GTATCATCTC TCTCTCTGAG TTGAACACAA		4764



TTC TTC AGG TTT GGT CCT ACA AAG TTT ACG CCT AAC 185	16 CTT AGT Phe Phe Arg Phe Val Pro Thr Lys Phe Thr Pro Asn 190	195 Leu Ser 200	6786
GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val 205	210 215		6834
GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu 220	225 230		6882
CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys 235	240 245		6930
ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTGTA CGATTTGTA Ile Ile Gln 250			6979
GTATCATCTC TCTCTCTGAG TTGAACACAA GGCTCCAGC CACATTCTTG GTCAAACCTTA CATTTCCTCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTG CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGTAGAATT ACAGTTGTGTG TTATTACTTT CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAACAA AAGTGATATA AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTGGG GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTCAAG ACCAGCCTGA CCAACATGGT GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG TACCACTAC TCAGGGCTGA GGCAGGAGAA TCGCTTGAAC CCAGGAGATG GAGGTTGCAG TGAGCTGAGA TTGTACCACT GCACTCCAGT CTGGCAACA GAGCAAGATT TCATCACACA CACACACACA CACACACACA CACACATTAG AAATGTGTAC TTGGCTTTGT TACCTATGGT ATTAGTGCAT CTATTGCATG GAACTTCAA GCTACTCTGG TTGTGTTAAG CTCTTCATTG GGTACAGGTC ACTAGTATTA AGTCAGGTT ATTGGATGC ATTCCACGGT AGTGATGACA ATTCACTCAGG CTAGTGTGTG TGTTCACCTT GTCACTCCCA CCACTAGACT AATCTCAGAC CTTCACTCAA AGACACATTA CACTAAAGAT GATTGCTTT TTTGTGTTA ATCAAGCAAT GGTATAAACC AGCTTGACTC TCCCCAAACA GTTTTCGTA CTACAAAGAA GTTTATGAAG CAGAGAAATG TGAATTGATA TATATATGAG ATTCTAACCC AGTTCCAGCA TTGTTTCATT GTGTAATTGA AATCATAGAC AAGCCATTAA AGCCTTGCT TTCTTATCTA AAAAAAAAAA AAAAAAAATG AAGGAAGGGG TATTAAAAGG AGTGATCAAA TTTTAACATT CTCTTAAATT AATTCAATTAA TAACTTTACT TTTTTTCATT TATTGTGCAC TTACTATGTG GTACTGTGCT ATAGAGGCTT TAACATTAT AAAAACACTG TGAAAGTTGC TTCAGATGAA TATAGGTAGT AGAACGGCAG AACTAGTATT CAAAGCCAGG TCTGATGAAT CCAAAAACAA ACACCCATTA CTCCCATTAA CTGGGACATA CTTACTCTAC CCAGATGCTC TGGGCTTTGT AATGCCTATG	75	8419	

TAAATAACAT AGTGTGTTGTTGGTTATTT TCCTATGTAA TGTCTAC	TATATCTGTA	8479
TCTATCTCTT GCTTCTTC CAAAGGTAAA CTATGTGTCT AAAATGTG	AAAAAATAAC	8539
ACACTATTCC AAATTACTGT TCAAATT CCT TTAAGTCAGT GATAATTATT	TGTTTGACA	8599
TTAACATGA AGTCCCTGT GGGTACTAGG TAAACCTTTA ATAGAATGTT AATGTTGTA	8659	
TTCATTATAA GAATTTTGG CTGTTACTTA TTTACAACAA TATTCAC	TAATTAGACA	8719
TTTACTAAC TTTCTCTTGA AAACAATGCC CAAAAAGAA CATTAGAAGA CACGTAAGCT	8779	
CAGTTGGTCT CTGCCACTAA GACCAGCCA CAGAAGCTTG ATTTTATTCA AACTTGCAT	8839	
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GAT ATT GAC CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT	9007	
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala		
255 260 265		
AAC CTC ACC TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA	9055	
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly		
270 275 280		
AAG AAA GTG GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA	9103	
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys		
285 290 295		
CCC AGT GAC CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT	9151	
Pro Ser Asp Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn		
300 305 310 315		
GGC GAC CAA GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA	9199	
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser		
320 325 330		
AAG ACG TAC CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC	9247	
Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr		
335 340 345		
ATC AGG TTC CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA	9295	
Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu		
350 355 360		
TTT TTA GAA ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC	9343	
Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys		
365 370 375		
TTA TAACTGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT	9396	
Leu		
380		
GGATGAGTAA ACTGTTCTC AGGCACCTGA GGCTTTCAGT GATATCTTC TCATTACAG	9456	
TGACTAATTT TGCCACAGGG TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT	9516	
CCTCCAATAA ACCCAAATG GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT	9576	
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CTCCACTGGG CCTTACTAAA TATGGGAATG TCTAACTTAA ATAGCTTGG GATTCCAGCT	9696	
ATGCTAGAGG CTTTATTAG AAAGCCATAT TTTTCTGT AAAAGTTACT AATATATCTG	9756	
TAACACTATT ACAGTATTGC TATTTATATT CATTAGATA TAAGATTTGG ACATATTATC	9816	

ATCCTATAAA GAA <del>T</del> ATAT GACTTAATTT TAGAAAGAAA ATTATAT <del>T</del>	GTTTATTATG	9876
ACAAATGAAA GAGA <del>A</del> ATAT ATATTTTAA TGGAAGTTT GTAGCAT <del>T</del>	TCTAATAGGT	9936
ACTGCCATAT TTTCTGTGT GGAGTATTTT TATAATTAA TCTGTATAAG CTGTAATATC		9996
ATTTATAGA AAATGCATTA TTTAGTCAAT TGTTAACATG TGAAAACAT ATGAAATATA		10056
AATTATCTGA ATATTAGATG CTCTGAGAAA TTGAATGTAC CTTATTAAAG AGATTTATG		10116
GTTTATAAC TATATAAATG ACATTATTAA AGTTTCAAA TTATTTTTA TTGCTTC		10176
TGTTGCTTTT ATTT		10190

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro		
-11 -10	-5	1 5
Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp		
10	15	20
Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp		
25	30	35
Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp		
40	45	50
His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
55	60	65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu		
70	75	80 85
Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg		
90	95	100
Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg		
105	110	115
Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr		
120	125	130
Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly		
135	140	145
Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser		
150	155	160 165
Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys		
170	175	180
Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn		
185	190	195
Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala		
200	205	210

Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Gln Gln Thr  
 215 220 225

Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile  
 230 235 240 245

Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln  
 250 255 260

Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu  
 265 270 275

Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys  
 280 285 290

Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser  
 295 300 305

Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met  
 310 315 320 325

His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr  
 330 335 340

Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr  
 345 350 355

Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln  
 360 365 370

Ser Val Lys Ile Ser Cys Leu  
 375 380

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..20
  - (D) OTHER INFORMATION: /note= "synthetic DNA (primer 2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CARGARCARA CNTTYCARYT

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..21
  - (D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

(xi) SEQUE DESCRIPTION: SEQ ID NO:108:

YTTRTACATN GTRAANSWRT G

21

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0